

OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/024,197

DATE: 01/14/2002

TIME: 18:21:46

Input Set : A:\PT0.VSK.txt

Output Set: N:\CRF3\01142002\J024197.raw

3 <110> APPLICANT: CANFIELD, William
 5 <120> TITLE OF INVENTION: HIGHLY PHOSPHORYLATED ACID BETA-GLUCOCEREBROSIDASE AND
 METHODS OF
 6 TREATING GAUCHER'S DISEASE
 8 <130> FILE REFERENCE: 209794US0
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/024,197
 C--> 10 <141> CURRENT FILING DATE: 2001-12-21
 10 <160> NUMBER OF SEQ ID NOS: 27
 12 <170> SOFTWARE: PatentIn version 3.1
 14 <210> SEQ ID NO: 1
 15 <211> LENGTH: 3600
 16 <212> TYPE: DNA
 17 <213> ORGANISM: hybrid
 19 <400> SEQUENCE: 1

ENTERED

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24 gttttgtttg attcctatag agacaatatt gctggaaagt cctttcagaa tcggctttgt      180
26 ctgcccattg cgattgacgt tgtttacacc tgggtgaatg gcacagatct tgaactactg      240
28 aaggaaactac agcaggctcag agaacagatg gaggaggagc agaaagcaat gagagaaatc      300
30 cttgggaaaa acacaacgga acctactaag aagagtgaga agcagttaga gtgtttgcta      360
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36 gcaaaaccaa aaaacccttc taccaatgtc tcagttgttg tttttgacag tactaaggat      540
38 gttgaagatg cccactctgg actgcttaaa ggaaatagca gacagacagt atggaggggc      600
40 tacttgacaa cagataaaga agtccctgga ttagtgctaa tgcaagattt ggctttcctg      660
42 agtggatttc caccaacatt caaggaaaca aatcaactaa aaacaaaatt gccagaaaat      720
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52 tactcattgc gatctatcga gaggcattgc ccattgggtc ggaatatatt cattgtcacc      1020
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76 gtagccaaaa gaggagttga aggtgcctat agtgacaatc caataattcg acatgcttct      1740
78 attgccaaac agtggaacac catccacctc ataatgcaca gtggaatgaa tgccaccaca      1800
80 atacatttta atctcacgtt tcaaaataca aacgatgaag agttcaaaaat gcagataaca      1860
82 gtggagggtg acacaagggg gggacccaaa ctgaattcta cgcccagaa gggttacgaa      1920
84 aatttagtta gtcccataac acttcttcca gaggcggaaa tcctttttga ggatattccc      1980
86 aaagaaaaac gcttcccga gtttaagaga catgatgtta actcaacaag gagagcccag      2040

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88 gaagagggtga aaattcccct ggtaaattatt tcaactccttc caaaagacgc ccagttgagt 2100
90 ctcaataacct tggatttgca actggaacat ggagacatca ctttgaaagg atacaatttg 2160
92 tccaagtcag ccttgctgag atcattttctg atgaactcac agcatgctaa aataaaaaat 2220
94 caagctataa taacagatga aacaaatgac agtttggtgg ctccacagga aaaacagggt 2280
96 cataaaagca tcttgccaaa cagcttagga gtgtctgaaa gattgcagag gttgactttt 2340
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100 gagaccacag caagatttag agtggaaact cacacccaaa aaaccatagg cggaaatgtg 2460
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106 ggcgttactg aagtgttact tggaagaaag ctgcagcatt acacagatag ttacttgggc 2640
108 tttttgccat gggagaaaaa aaagtatttc ctagatcttc tcgacgaaga agagtcatgt 2700
110 aagacacaat tggcctactt cactgatagc aagaatagag ccagatacaa gagagataca 2760
112 tttgcagatt ccctcagata tgtaaataaa attctaaata gcaagtttggt attcacatcg 2820
114 cggaaagtcc ctgctcacat gcctcacatg attgaccgga ttgttatgca agaactgcaa 2880
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132 tctcatgtgg ttggccagtt ggatgacata agaaaaaacc ctaggaagtt tgtttgcctg 3420
134 aatgacaaca ttgaccacaa tcataaagat gctcagacag tgaaggctgt tctcagggac 3480
136 ttctatgaat ccatgttccc cataccttcc caatttgaac tgccaagaga gtatcgaaac 3540
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141 <210> SEQ ID NO: 2

142 <211> LENGTH: 1199

143 <212> TYPE: PRT

144 <213> ORGANISM: hybrid

146 <400> SEQUENCE: 2

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152 Gly Ser Thr Gly Asp Glu Asp Gln Val Asp Pro Arg Leu Ile Asp Gly
153 20 25 30
156 Lys Leu Ser Arg Asp Gln Tyr His Val Leu Phe Asp Ser Tyr Arg Asp
157 35 40 45
160 Asn Ile Ala Gly Lys Ser Phe Gln Asn Arg Leu Cys Leu Pro Met Pro
161 50 55 60
164 Ile Asp Val Val Tyr Thr Trp Val Asn Gly Thr Asp Leu Glu Leu Leu
165 65 70 75 80
168 Lys Glu Leu Gln Gln Val Arg Glu Gln Met Glu Glu Glu Gln Lys Ala
169 85 90 95
172 Met Arg Glu Ile Leu Gly Lys Asn Thr Thr Glu Pro Thr Lys Lys Ser
173 100 105 110
176 Glu Lys Gln Leu Glu Cys Leu Leu Thr His Cys Ile Lys Val Pro Met
177 115 120 125
180 Leu Val Leu Asp Pro Ala Leu Pro Ala Asn Ile Thr Leu Lys Asp Leu
181 130 135 140

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184 Pro Ser Leu Tyr Pro Ser Phe His Ser Ala Ser Asp Ile Phe Asn Val
185 145 150 155 160
188 Ala Lys Pro Lys Asn Pro Ser Thr Asn Val Ser Val Val Val Phe Asp
189 165 170 175
192 Ser Thr Lys Asp Val Glu Asp Ala His Ser Gly Leu Leu Lys Gly Asn
193 180 185 190
196 Ser Arg Gln Thr Val Trp Arg Gly Tyr Leu Thr Thr Asp Lys Glu Val
197 195 200 205
200 Pro Gly Leu Val Leu Met Gln Asp Leu Ala Phe Leu Ser Gly Phe Pro
201 210 215 220
204 Pro Thr Phe Lys Glu Thr Asn Gln Leu Lys Thr Lys Leu Pro Glu Asn
205 225 230 235 240
208 Leu Ser Ser Lys Val Lys Leu Leu Gln Leu Tyr Ser Glu Ala Ser Val
209 245 250 255
212 Ala Leu Leu Lys Leu Asn Asn Pro Lys Asp Phe Gln Glu Leu Asn Lys
213 260 265 270
216 Gln Thr Lys Lys Asn Met Thr Ile Asp Gly Lys Glu Leu Thr Ile Ser
217 275 280 285
220 Pro Ala Tyr Leu Leu Trp Asp Leu Ser Ala Ile Ser Gln Ser Lys Gln
221 290 295 300
224 Asp Glu Asp Ile Ser Ala Ser Arg Phe Glu Asp Asn Glu Glu Leu Arg
225 305 310 315 320
228 Tyr Ser Leu Arg Ser Ile Glu Arg His Ala Pro Trp Val Arg Asn Ile
229 325 330 335
232 Phe Ile Val Thr Asn Gly Gln Ile Pro Ser Trp Leu Asn Leu Asp Asn
233 340 345 350
236 Pro Arg Val Thr Ile Val Thr His Gln Asp Val Phe Arg Asn Leu Ser
237 355 360 365
240 His Leu Pro Thr Phe Ser Ser Pro Ala Ile Glu Ser His Val His Arg
241 370 375 380
244 Ile Glu Gly Leu Ser Gln Lys Phe Ile Tyr Leu Asn Asp Asp Val Met
245 385 390 395 400
248 Phe Gly Lys Asp Val Trp Pro Asp Asp Phe Tyr Ser His Ser Lys Gly
249 405 410 415
252 Gln Lys Val Tyr Leu Thr Trp Pro Val Pro Asn Cys Ala Glu Gly Cys
253 420 425 430
256 Pro Gly Ser Trp Ile Lys Asp Gly Tyr Cys Asp Lys Ala Cys Asn Asn
257 435 440 445
260 Ser Ala Cys Asp Trp Asp Gly Gly Asp Cys Ser Gly Asn Ser Gly Gly
261 450 455 460
264 Ser Arg Tyr Ile Ala Gly Gly Gly Gly Thr Gly Ser Ile Gly Val Gly
265 465 470 475 480
268 Gln Pro Trp Gln Phe Gly Gly Gly Ile Asn Ser Val Ser Tyr Cys Asn
269 485 490 495
272 Gln Gly Cys Ala Asn Ser Trp Leu Ala Asp Lys Phe Cys Asp Gln Ala
273 500 505 510
276 Cys Asn Val Leu Ser Cys Gly Phe Asp Ala Gly Asp Cys Gly Gln Asp
277 515 520 525
280 His Phe His Glu Leu Tyr Lys Val Ile Leu Leu Pro Asn Gln Thr His

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281      530      535      540
284 Tyr Ile Ile Pro Lys Gly Glu Cys Leu Pro Tyr Phe Ser Phe Ala Glu
285 545      550      555      560
288 Val Ala Lys Arg Gly Val Glu Gly Ala Tyr Ser Asp Asn Pro Ile Ile
289      565      570      575
292 Arg His Ala Ser Ile Ala Asn Lys Trp Lys Thr Ile His Leu Ile Met
293      580      585      590
296 His Ser Gly Met Asn Ala Thr Thr Ile His Phe Asn Leu Thr Phe Gln
297      595      600      605
300 Asn Thr Asn Asp Glu Glu Phe Lys Met Gln Ile Thr Val Glu Val Asp
301      610      615      620
304 Thr Arg Glu Gly Pro Lys Leu Asn Ser Thr Ala Gln Lys Gly Tyr Glu
305 625      630      635      640
308 Asn Leu Val Ser Pro Ile Thr Leu Leu Pro Glu Ala Glu Ile Leu Phe
309      645      650      655
312 Glu Asp Ile Pro Lys Glu Lys Arg Phe Pro Lys Phe Lys Arg His Asp
313      660      665      670
316 Val Asn Ser Thr Arg Arg Ala Gln Glu Glu Val Lys Ile Pro Leu Val
317      675      680      685
320 Asn Ile Ser Leu Leu Pro Lys Asp Ala Gln Leu Ser Leu Asn Thr Leu
321      690      695      700
324 Asp Leu Gln Leu Glu His Gly Asp Ile Thr Leu Lys Gly Tyr Asn Leu
325 705      710      715      720
328 Ser Lys Ser Ala Leu Leu Arg Ser Phe Leu Met Asn Ser Gln His Ala
329      725      730      735
332 Lys Ile Lys Asn Gln Ala Ile Ile Thr Asp Glu Thr Asn Asp Ser Leu
333      740      745      750
336 Val Ala Pro Gln Glu Lys Gln Val His Lys Ser Ile Leu Pro Asn Ser
337      755      760      765
340 Leu Gly Val Ser Glu Arg Leu Gln Arg Leu Thr Phe Pro Ala Val Ser
341      770      775      780
344 Val Lys Val Asn Gly His Asp Gln Gly Gln Asn Pro Pro Leu Asp Leu
345 785      790      795      800
348 Glu Thr Thr Ala Arg Phe Arg Val Glu Thr His Thr Gln Lys Thr Ile
349      805      810      815
352 Gly Gly Asn Val Thr Lys Glu Lys Pro Pro Ser Leu Ile Val Pro Leu
353      820      825      830
356 Glu Ser Gln Met Thr Lys Glu Lys Lys Ile Thr Gly Lys Glu Lys Glu
357      835      840      845
360 Asn Ser Arg Met Glu Glu Asn Ala Glu Asn His Ile Gly Val Thr Glu
361      850      855      860
364 Val Leu Leu Gly Arg Lys Leu Gln His Tyr Thr Asp Ser Tyr Leu Gly
365 865      870      875      880
368 Phe Leu Pro Trp Glu Lys Lys Lys Tyr Phe Leu Asp Leu Leu Asp Glu
369      885      890      895
372 Glu Glu Ser Leu Lys Thr Gln Leu Ala Tyr Phe Thr Asp Ser Lys Asn
373      900      905      910
376 Arg Ala Arg Tyr Lys Arg Asp Thr Phe Ala Asp Ser Leu Arg Tyr Val
377      915      920      925

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380 Asn Lys Ile Leu Asn Ser Lys Phe Gly Phe Thr Ser Arg Lys Val Pro
381      930                      935                      940
384 Ala His Met Pro His Met Ile Asp Arg Ile Val Met Gln Glu Leu Gln
385 945                      950                      955                      960
388 Asp Met Phe Pro Glu Glu Phe Asp Lys Thr Ser Phe His Lys Val Arg
389                      965                      970                      975
392 His Ser Glu Asp Met Gln Phe Ala Phe Ser Tyr Phe Tyr Tyr Leu Met
393                      980                      985                      990
396 Ser Ala Val Gln Pro Leu Asn Ile Ser Gln Val Phe Asp Glu Val Asp
397      995                      1000                      1005
400 Thr Asp Gln Ser Gly Val Leu Ser Asp Arg Glu Ile Arg Thr Leu
401      1010                      1015                      1020
404 Ala Thr Arg Ile His Glu Leu Pro Leu Ser Leu Gln Asp Leu Thr
405      1025                      1030                      1035
408 Gly Leu Glu His Met Leu Ile Asn Cys Ser Lys Met Leu Pro Ala
409      1040                      1045                      1050
412 Asp Ile Thr Gln Leu Asn Asn Ile Pro Pro Thr Gln Glu Ser Tyr
413      1055                      1060                      1065
416 Tyr Asp Pro Asn Leu Pro Pro Val Thr Lys Ser Leu Val Thr Asn
417      1070                      1075                      1080
420 Cys Lys Pro Val Thr Asp Lys Ile His Lys Ala Tyr Lys Asp Lys
421      1085                      1090                      1095
424 Asn Lys Tyr Arg Phe Glu Ile Met Gly Glu Glu Glu Ile Ala Phe
425      1100                      1105                      1110
428 Lys Met Ile Arg Thr Asn Val Ser His Val Val Gly Gln Leu Asp
429      1115                      1120                      1125
432 Asp Ile Arg Lys Asn Pro Arg Lys Phe Val Cys Leu Asn Asp Asn
433      1130                      1135                      1140
436 Ile Asp His Asn His Lys Asp Ala Gln Thr Val Lys Ala Val Leu
437      1145                      1150                      1155
440 Arg Asp Phe Tyr Glu Ser Met Phe Pro Ile Pro Ser Gln Phe Glu
441      1160                      1165                      1170
444 Leu Pro Arg Glu Tyr Arg Asn Arg Phe Leu His Met His Glu Leu
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449      1190                      1195
452 <210> SEQ ID NO: 3
453 <211> LENGTH: 5597
454 <212> TYPE: DNA
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462 ggcggctcag gctcctcggg gcgtggcgtg gcggtgaagg ggtgatgctg ttcaagctcc      180
464 tgcagagaca aacctatacc tgctgtcccc acaggtatgg gctctacgtg tgcttcttgg      240
466 gcgtcgttgt caccatcgtc tccgccttcc agttcggaga ggtggttctg gaatggagcc      300
468 gagatcaata ccatgttttg tttgattcct atagagacaa tattgctgga aagtcctttc      360
470 agaatcggct ttgtctgccc atgccgattg acgttggtta cacctgggtg aatggcacag      420
472 atcttgaact actgaaggaa ctacagcagg tcagagaaca gatggaggag gaggagaaag      480

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Use of n and/or Xaa has been detected in the Sequence Listing.
 Review the Sequence Listing to insure a corresponding
 explanation is presented in the <220> to <223> fields of
 each sequence using n or Xaa.

VERIFICATION SUMMARY

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L:10 M:270 C: Current Application Number differs, Replaced Current Application No
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:1640 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:1926 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:1930 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:1932 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15